

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:25:09 ; Search time 47 Seconds

Title: US-10-634-027-7

Perfect score: 1744

Sequence: 1 GQPLSHIQLGQKGRKTS VRDVLPARKLRSSEQHHHH 319

Scoring table: BIOSUM62

Gapext: 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued_Patents_AA:*

1: /cgn2_5/prodata/1/1aa/5_COMB.pep:*

2: /cgn2_5/prodata/1/1aa/6_COMB.pep:*

3: /cgn2_5/prodata/1/1aa/7_COMB.pep:*

4: /cgn2_5/prodata/1/1aa/8_COMB.pep:*

5: /cgn2_5/prodata/1/1aa/RE_COMB.pep:*

6: /cgn2_5/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query %

Match Length DB ID Description

Result No.	Score	Query	%	Match Length	DB ID	Description
1	1691	97.0	1997	2	US-09-949-016-6275	Sequence 6275, Ap
2	1644	94.3	1993	2	US-09-949-016-6049	Sequence 8049, Ap
3	1444	82.8	278	1	US-09-201-697-16	Sequence 16, Ap
4	1374	78.8	254	1	US-09-685-932-14	Sequence 14, Ap
5	1374	78.8	254	1	US-09-144-925-14	Sequence 2, Ap
6	878.5	50.4	1357	2	US-09-854-585-2	Sequence 2, Ap
7	878.5	50.4	1337	2	US-09-447-533-2	Sequence 2, Ap
8	878.5	50.4	1337	4	PCT-US95-05512.2	Sequence 2, Ap
9	843.5	273	1	US-09-201-637-17	Sequence 17, Ap	
10	765	43.9	843	2	US-09-949-016-8833	Sequence 883, Ap
11	765	43.9	506	2	US-09-949-016-8834	Sequence 883, Ap
12	765	43.9	506	2	US-09-949-016-8835	Sequence 883, Ap
13	765	43.9	506	2	US-09-949-016-8836	Sequence 883, Ap
14	765	43.9	506	2	US-09-949-016-8837	Sequence 883, Ap
15	765	43.9	506	2	US-09-949-016-8838	Sequence 883, Ap
16	765	43.9	1214	2	US-09-949-016-8828	Sequence 882, Ap
17	765	43.9	1224	2	US-09-949-016-8829	Sequence 882, Ap
18	765	43.9	1274	2	US-09-949-016-8830	Sequence 883, Ap
19	765	43.9	1274	2	US-09-949-016-8831	Sequence 883, Ap
20	765	43.9	1274	2	US-09-949-016-8832	Sequence 883, Ap
21	765	43.9	1188	1	US-09-201-537-4	Sequence 4, Ap
22	761.5	43.7	1446	2	US-09-949-016-8051	Sequence 8051, Ap
23	761.5	43.7	1246	2	US-09-949-016-8052	Sequence 8052, Ap
24	761.5	43.7	1246	2	US-09-949-016-8053	Sequence 8053, Ap
25	761.5	43.7	1246	2	US-09-949-016-8054	Sequence 8054, Ap
26	761.5	43.7	1246	2	US-09-949-016-8055	Sequence 8055, Ap
27	760.5	1187	1	US-09-201-637-2	Sequence 2, Ap	

ALIGNMENTS

28	744.5	42.7	251	1	US-09-685-932-15	Sequence 15, Ap
29	744.5	42.7	251	1	US-09-144-923-15	Sequence 15, Ap
30	697.5	40.0	1711	1	US-09-342-930-2	Sequence 2, Ap
31	673	38.7	2301	2	US-09-822-871-4	Sequence 4, Ap
32	673	38.6	401	2	US-09-361-968-15	Sequence 15, Ap
33	673	38.6	402	1	US-09-036-21-15	Sequence 15, Ap
34	673	38.6	402	1	US-09-449-609-15	Sequence 22, Ap
35	673	38.6	898	1	US-09-036-21-10-22	Sequence 22, Ap
36	673	38.6	898	1	US-09-449-609-22	Sequence 22, Ap
37	673	38.6	898	2	US-09-361-968-22	Sequence 47, Ap
38	667	38.2	289	2	US-09-361-968-47	Sequence 11, Ap
39	667	38.2	322	1	US-09-449-609-11	Sequence 11, Ap
40	667	38.2	322	2	US-09-822-871-2	Sequence 2, Ap
41	667	38.2	322	2	US-09-968-11	Sequence 16, Ap
42	658	37.7	2291	2	US-09-968-11	Sequence 16, Ap
43	633.5	36.9	255	1	US-09-968-932-16	Sequence 2, Ap
44	633.5	36.9	255	1	US-09-144-923-16	Sequence 16, Ap
45	618.5	35.5	2314	2	US-09-816-703A-2	Sequence 2, Ap

Db 1962 DVLRARKRSOEQN 1975

RESULT 2
US-09-949-016-8049
Sequence 8049, Application US/09949016
Patient No. 6812319
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIORITY APPLICATION NUMBER: 60/141, 755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237, 768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231, 498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 8049
LENGTH: 1903
TYPE: PRT
ORGANISM: Human
US-09-949-016-8049

Query Match 94.3%; Score 1644; DB 2; Length 1903;
Best Local Similarity 97.5%; Pred. No. 7-e-15; Mismatches 306; Conservative 1; Indels 6; Gaps 1; Matches 306; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 2 DRPDSVHNLGONGNFKTSQPIKINPQEGFMKQASNSVYLSKEYELKVGNGQSDI 61
Db 1574 DRPLSVHNLGOKGK-----PIKINPQEGFMKQASNSVYLSKEYELKVGNGQSDI 1627

QY 62 ALLPENRGSKRYNINLPIPATRKLNSVDDPDCSDYKINASVYLSKEYELKVGNGQSDI 121
Db 1628 ALLPENRGSKRYNINLPIPATRKLNSVDDPDCSDYKINASVYLSKEYELKVGNGQSDI 1687

QY 122 TKDPPWQKWMQEVNNTIVMTCQEVKGRVCDHWMPPADSSLYGDPITLQMSLSEPUW 181
Db 1688 TKDPPWQKWMQEVNNTIVMTCQEVKGRVCDHWMPPADSSLYGDPITLQMSLSEPUW 1747

QY 182 TIREFKCGESEGDALRHLRHFYTWDPDGVPETTOSLQFQFVTDYINRSPGAGTV 241
Db 1748 TIREFKCGESEGDALRHLRHFYTWDPDGVPETTOSLQFQFVTDYINRSPGAGTV 1807

QY 242 VHCGAGYVORTGFIADRLQQLDSKDSVYIAGVHDLRHLRHMVTECOVYVHQVR 301
Db 302 DVLRARKRSOEQN 315
QY 1808 VHCGAGYVORTGFIADRLQQLDSKDSVYIAGVHDLRHLRHMVTECOVYVHQVR 1867
Db 1868 DVLRARKRSOEQN 1881

RESULT 3
US-08-001-697-16
Sequence 16, Application US/08201697
Patient No. 5705623
GENERAL INFORMATION:
APPLICANT: Wiggins, Roger C.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
TITLE OF INVENTION: 1
NUMBER OF SEQ ID NOS: 17
CORRESPONDENCE ADDRESS:
APPLICANT: Thomas, Peedikail B.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
TITLE OF INVENTION: 1
NUMBER OF SEQ ID NOS: 17
CITY: San Diego
STATE: California

RESULT 4
US-08-685-992-14
Sequence 14, Application US/08685992
Patient No. 5912138
GENERAL INFORMATION:
APPLICANT: Flint, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQ ID NOS: 36
CORRESPONDENCE ADDRESS: ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201, 697
FILING DATE: 25-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Christopher A.
REGISTRATION NUMBER: 31, 815
REFERENCE/DOCKET NUMBER: P-UM 9783
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-201-697-16
Query Match 82.8%; Score 1444; DB 1; Length 278;
Best Local Similarity 95.7%; Pred. No. 6.9-e-145; Mismatches 266; Conservative 5; Indels 0; Gaps 0; Matches 266; Conservative 5; Mismatches 7;

QY 22 PIKINPQEGFMKQASNSVYLSKEYELKVGNGQSDI 81
Db 1 PIKINPQEGFMKQASNSVYLSKEYELKVGNGQSDI 60

QY 82 TRYKLSVNDPDSQVYIARNARRELYIVQPLRGKUDWMQMMEDQHILMV 1411
Db 61 TRYKLSVNDPDSQVYIARNARRELYIVQPLRGKUDWMQMMEDQHILMV 1207

QY 142 TOCVEKGRVCDHWMPPADSSLYGDPITLQMSLSEPUWTFREKCGESEGDALRHLRHFYTWDPDGVPETTOSLQFQFVTDYINRSPGAGTV 2011
Db 121 TOCVEKGRVCDHWMPPADSSLYGDPITLQMSLSEPUWTFREKCGESEGDALRHLRHFYTWDPDGVPETTOSLQFQFVTDYINRSPGAGTV 1800

QY 202 HFPHTYTWDPDGVPETTOSLQFQFVTDYINRSPGAGTVHCSAGWRTGTFIALDRL 2611
Db 181 HFPHTYTWDPDGVPETTOSLQFQFVTDYINRSPGAGTVHCSAGWRTGTFIALDRL 2400

QY 262 QQLDSKDSVYIAGVHDLRHLRHMVTECOVYVHQVR 299
Db 241 QQLDSKDSVYIAGVHDLRHLRHMVTECOVYVHQVR 279

APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHL96-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEX: 781-861-9540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 254 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-685-992-14

Query Match 78.8%; Score 1374; DB 1; Length 254;
 Best Local Similarity 99.2%; Pred. No. 1.6e-13; 0; Mismatches 0; Indels 2; Gaps 1;
 Matches 254; Conservative 0;

QY 56 NSCDIALIPENKGKRYNINLPDAIRVKEVGRKWDHPPADODSLIGDILQMLSE 115
 1 NSCDIALIPENKGKRYNINLPDAIRVKEVGRKWDHPPADODSLIGDILQMLSE 115

QY 116 QGPLGKTDKFWMQWNEQNTNNTWVTOCQEKGKWDHPPADODSLIGDILQMLSE 175
 61 QGPLGKTDKFWMQWNEQNTNNTWVTOCQEKGKWDHPPADODSLIGDILQMLSE 120

QY 176 SVLPETRIRPSKICGEGQDAAHLIRIIPHYTWDHGPPETOSLQFVRTVTDYINRSP 235
 121 SVLPETRIRPSKICGEGQDAAHLIRIIPHYTWDHGPPETOSLQFVRTVTDYINRSP 178

QY 236 GAGPTVHSAAGVGRGTCFALDRILQOLQSKSDSYDQVHDLRHRVHMQTEQVY 295
 179 GAGPTVHSAAGVGRGTCFALDRILQOLQSKSDSYDQVHDLRHRVHMQTEQVY 238

QY 296 LHQCVRDYVARKRS 311
 239 LHQCVRDYVARKRS 254

RESULT 5
 US-09-144-925-14
 Sequence 14 Application US/09144925
 Patent No. 505179
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 ATTORNEY: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02421-4799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,585
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/237,940
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

RESULT 6 US-08-854-585-2
 US-08-854-585-2
 Sequence 2, Application US/08854585
 Patent No. 611410
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K. and strnan, Arne
 TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, Suite 6300
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,585
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/237,940
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27866/31954
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 LENGTH: 1337 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 LENGTH: 1337 amino acids
 TOPLOGY: linear
 MOLECULE TYPE: protein

US-08-584-585-2

Query Match Similarity 50.4%; Score 878.5; DB 2; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 9e-84; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKIKNQFQGHFMKLOADSNYLISKEYEELKDVGRNOSCDIALPENGGKRYNIL 77
 1016 KKSCKIKNQFQGHFMKLOADSNYLISKEYEELKDVGRNOSCDIALPENGGKRYNIL 1075

Db 78 PYDATRVKLSNVDPPCSOYINASXPGNNFRKYYTQGQPLTKDPMWQMEQHN 137
 1076 PYDISRKLS-VQHSTDDYIYANMPGYSKDKTATQPLPMLQDFWMWNEKNTYA 1134

QY 1076 PYDISRKLS-VQHSTDDYIYANMPGYSKDKTATQPLPMLQDFWMWNEKNTYA 1134

Db 138 IVMVQCKVGRKVKHPPADSIKSLDILQMSSESLPENTIREKIGEQLDHA 197
 1135 IIMLKCKVQGRKTCKEYWSKQ-AQDYGDTIVMTSEIVLPEWVIRDFVKNQTSBH 1193

QY 198 RLIRHFTWMDHGPEPTOSIYQFRTRDYNRSPGAGPTVHSSAGYGRGTFAL 257
 1194 PL-ROFHTSWMDHGPDITDILINRYLDRMKQSPSPSPILVHSSAGYGRGTFAL 1252

Db 258 DRIQQLQSKSDVYGAHVDLRHRVHMQTCQYYLHQCYRDVLRARK 308
 1253 DRILYQIENENTDVQYDVGIVIDLRMRPLMVQTDQVFLNQCVLIVSOK 1303

RESULT 7

US-09-47-533-2

Sequence 2, Application US/09447533
 Patent No. 6552169
 GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K.
 INVENTOR: Ostrman, Arne

TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE PHOSPHATASE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed IP Law Group PLLC
 STREET: Suite 6300, 701 Fifth Avenue
 CITY: Seattle, Washington
 STATE: Washington
 COUNTRY: USA
 ZIP: 9810104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatientIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/447,533
 FILING DATE: 23-NO-1999
 ATTORNEY/AGENT INFORMATION:
 NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1337 amino acids
 TYPE: amino acid
 LENGTH: 1337 amino acids
 TOPLOGY: linear
 MOLECULE TYPE: protein

US-09-447-533-2

Query Match Similarity 50.4%; Score 878.5; DB 2; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 9e-84; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKIKNQFQGHFMKLOADSNYLISKEYEELKDVGRNOSCDIALPENGGKRYNIL 77

Db 1016 KKSCKIKNQFQGHFMKLOADSNYLISKEYEELKDVGRNOSCDIALPENGGKRYNIL 1075

QY 78 PYDATRVKLSNVDPPCSOYINASXPGNNFRKYYTQGQPLTKDPMWQMEQHN 137

Db 1076 PYDISRKLS-VQHSTDDYIYANMPGYSKDKTATQPLPMLQDFWMWNEKNTYA 1134

QY 138 IVMVQCKVGRKVKHPPADSIKSLDILQMSSESLPENTIREKIGEQLDHA 197

Db 1135 IIMLKCKVQGRKTCKEYWSKQ-AQDYGDTIVMTSEIVLPEWVIRDFVKNQTSBH 1193

QY 198 RLIRHFTWMDHGPEPTOSIYQFRTRDYNRSPGAGPTVHSSAGYGRGTFAL 257

Db 1194 PL-ROFHTSWMDHGPDITDILINRYLDRMKQSPSPSPILVHSSAGYGRGTFAL 1252

RESULT 8

PCT-US95-05512-2

Sequence 2, Application PCT/US9505512

GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas K. and Ostrman, Arne

TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 233 South Wacker Drive, Suite 6300
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatientIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05512

FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Borun, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1337 amino acids
 TYPE: amino acid
 LENGTH: 1337 amino acids
 TOPLOGY: linear
 MOLECULE TYPE: protein

PCT-US95-05512-2

Query Match Similarity 50.4%; Score 878.5; DB 4; Length 1337;

INFORMATION FOR SEQ ID NO: 2:

Patent No. 6811339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C1001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8835
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-8834

Query Match 43.9%; Score 765; DB 2; Length 506;
 Best Local Similarity 48.2%; Pred. No. 2,3e-2; Matches 147; Conservative 48.2%; Pred. No. 2,3e-2; Mismatches 89; Indels 10; Gaps 4;
 Matches 147; Conservative 48.2%; Mismatches 89; Indels 10; Gaps 4;
 Qy 2 DRPLSIVHNLGOKG--NRTKSCPKINKPESHFMKLOADSNYLSEKYLKGVRGQS 58
 Db 184 DYLLAFYINPWSKNGKKGKLNTPVOLDDFDAYIKOMAKOSDKFSQFEBKLIGLDIP 243
 Qy 59 CDIAALPENGRKRNLYPDATYKUSNVDDPESDYNASTIPSNFREYIVTQGP 118
 Db 244 HFAADLPKRCRKTINLPLPSRKRVSRLVMSNESEGADYINANIPGNSPQVIATQGP 303
 Db 119 LPGTQDKDFRTMWEQHVNIVMVTQCEVKGRVKCSDHMPADQSLYYQDILQMSSESVL 178
 Qy 184 DYLLAFYINPWSKNGKKGKLNTPVOLDDFDAYIKOMAKOSDKFSQFEBKLIGLDIP 243
 Qy 59 CDIAALPENGRKRNLYPDATYKUSNVDDPESDYNASTIPSNFREYIVTQGP 118
 Db 244 HFAADLPKRCRKTINLPLPSRKRVSRLVMSNESEGADYINANIPGNSPQVIATQGP 303
 Db 364 DDWACRHERI--NVADEMQDMHVNTPWMPDQHGPVANAEASLQFVHMTRQMTKS-- 418
 Qy 237 AGPTVWCHSAGVGRGTFMADLILQQLSKSDVYQDATHDRLHRHMYWPTESQVYWL 296
 Db 419 KGPMLIHCASAGVGRGTFMADLILQQLSKSDVYQDATHDRLHRHMYWPTESQVYWL 363
 Db 364 LPETRNDFKMQLQKQSQIVMLTQNEKGRVKCSDHMPADQSLYYQDILQMSSESVL 178
 Qy 179 PEWTIREKICGEEBOLDAHRLLRHFIITWPDHGP--ETQSLIQFRTTRDYNRPG 236
 Db 297 HQCVR 301
 Db 479 HQCVO 483
 RESULT 13
 US-09-949-016-8835
 Sequence 8835, Application US/09949016
 Patent No. 6811339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C1001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8835
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-8836

Query Match 43.9%; Score 765; DB 2; Length 506;
 Best Local Similarity 48.2%; Pred. No. 2,3e-2; Matches 147; Conservative 48.2%; Pred. No. 2,3e-2; Mismatches 89; Indels 10; Gaps 4;
 Matches 147; Conservative 48.2%; Mismatches 89; Indels 10; Gaps 4;
 Qy 2 DRPLSIVHNLGOKG--NRTKSCPKINKPESHFMKLOADSNYLSEKYLKGVRGQS 58
 Db 184 DYLLAFYINPWSKNGKKGKLNTPVOLDDFDAYIKOMAKOSDKFSQFEBKLIGLDIP 243
 Qy 59 CDIAALPENGRKRNLYPDATYKUSNVDDPESDYNASTIPSNFREYIVTQGP 118
 Db 244 HFAADLPKRCRKTINLPLPSRKRVSRLVMSNESEGADYINANIPGNSPQVIATQGP 303
 Db 119 LPGTQDKDFRTMWEQHVNIVMVTQCEVKGRVKCSDHMPADQSLYYQDILQMSSESVL 178
 Qy 184 DYLLAFYINPWSKNGKKGKLNTPVOLDDFDAYIKOMAKOSDKFSQFEBKLIGLDIP 243
 Qy 59 CDIAALPENGRKRNLYPDATYKUSNVDDPESDYNASTIPSNFREYIVTQGP 118
 Db 244 HFAADLPKRCRKTINLPLPSRKRVSRLVMSNESEGADYINANIPGNSPQVIATQGP 303
 Db 364 LPETRNDFKMQLQKQSQIVMLTQNEKGRVKCSDHMPADQSLYYQDILQMSSESVL 178
 Qy 119 LPGTQDKDFRTMWEQHVNIVMVTQCEVKGRVKCSDHMPADQSLYYQDILQMSSESVL 178
 Db 364 LPETRNDFKMQLQKQSQIVMLTQNEKGRVKCSDHMPADQSLYYQDILQMSSESVL 178
 LENGTH: 506
 TYPE: PRT

QY 179 PENTIREPKCGEGEOLDAHRLIRPHYTWMDHGP- -ETTOSLIQFVPTVDRYINRSPG 236
 Db 364 DDWACHFRI-- NYADEMDOMVNTYAWDHGIFTANAAEBSILOFVNMVRQATKS-- 418
 QY 237 AGPTVHCSAGVGTGTFIALDRILQOQDSKDSVYIYGAHDLRIRVHMTQECQVYL 296
 Db 419 KGPMLIHCSAGVGTGTFIALDRILQHIRDHFVOLGIVLSMRSYMSMVQTEQYIFI 478
 QY 297 HCQVR 301
 Db 479 HCQVQ 483

RESULT 14

US-09-949-016-8837
 Sequence 8837, Application US/09949016

; Sequence No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; PRIORITY NUMBER: 6/231,755

; PRIORITY FILING DATE: 2000-10-20

; PRIORITY FILING NUMBER: 60/231,768

; PRIORITY FILING DATE: 2000-10-03

; PRIORITY FILING NUMBER: 60/231,498

; PRIORITY FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; NUMBER OF SEQ ID NOS: 207012

; LENGTH: 506

; SEQ ID NO: 8838

; TYPE: PRT

; ORGANISM: Human

; US-09-949-016-8838

; Query Match

; Best Local Similarity

; Score

; DB

; 2

; DRPLSVHNLGOKO--NRKUSCPKINQFEGHMKLQDSNLYLSKEYELKDGNOQ 58

; Db

; 184

; DYLAFYTPNPKNGLKRKLTQVQDFFDAYIKRMDKSDYKESLQPEELKLIGDIP 243

; QY

; 59

; CDAIULPENGRKQYNNLIPIDATRVLKSNWDDPSDQVINAISVYQGPNFRRQXIVQGP 118

; Db

; 244

; HFAADLPLNRCRKYNTTLPDFSRVRLVSHNEEGADYINANVYQGP 303

; QY

; 119

; LPGTKDFKQWVQHNTTNTWQYCEKGVWQDHYPAQDLSYQGDLIQLQMSVSL 178

; Db

; 304

; LPETRNDPQWQVQLOQSKQITMLQTCNEKRRKHCYHPTFEPYQGTTWEMISEEQ 363

; QY

; 179

; PENTIREPKCGEGEOLDAHRLIRPHYTWMDHGP- -ETTOSLIQFVPTVDRYINRSPG 236

; Db

; 364

; DDWACHFRI-- NYADEMDOMVNTYAWDHGIFTANAAEBSILOFVNMVRQATKS-- 418

; QY

; 237

; AGPTVHCSAGVGTGTFIALDRILQOQDSKDSVYIYGAHDLRIRVHMTQECQVYL 296

; Db

; 419

; KGPMLIHCSAGVGTGTFIALDRILQHIRDHFVOLGIVLSMRSYMSMVQTEQYIFI 478

; QY

; 297

; HCQVR 301

; Db

; 479

; HCQVQ 483

; Search completed: February 17, 2006, 01:26:31

; Job time : 48 secs

; RESULT 15

; US-9-949-016-8838

; Sequence 8838, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

RESULT 2
 US-10-634-027-4
 ; Sequence 4, Application US/10634027
 ; Publication No. US20040077065A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Procter & Gamble Company
 ; APPLICANT: Evdokimov, Arrem G
 ; APPLICANT: Pokross, Matthew E
 ; TITLE OF INVENTION: Three Dimensional Coordinates of HPTPbeta
 ; FILE REFERENCE: 9045M2
 ; CURRENT APPLICATION NUMBER: US/10/634,027
 ; CURRENT FILING DATE: 2003-08-04
 ; PRIOR APPLICATION NUMBER: US 60/413,547
 ; PRIOR FILING DATE: 2002-09-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO: 4
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-634-027-4

Query Match 97.0%; Score 1691; DB 3; Length 1997;
 Best Local Similarity 99.4%; Pred. No. 3; e-152; Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DRPLSVHNLGOKGNRKTSCKPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQCDI 61
 Db 1662 DRPLSVHNLGOKGNRKTSCKPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQCDI 1721
 Qy 62 ALLPENRGKRNLYNLPYDATRKVLNSVDDPSDSDTINASYIQQNRRRTIVTQGPGLP 121
 Db 1722 ALLPENRGKRNLYNLPYDATRKVLNSVDDPSDSDTINASYIQQNRRRTIVTQGPGLP 1781
 Qy 122 TDKDPKWVQWVQVNVNITWQCVGKRCYWDQDSDVQGLP 181
 Db 1782 TDKDPKWVQWVQVNVNITWQCVGKRCYWDQDSDVQGLP 1841
 Qy 182 TIRPKKIGEOLDARLIRRHYTWPDHGVPETTOSLIQFRTRDYNIRSAGPTV 241
 Db 1842 TIRPKKIGEOLDARLIRRHYTWPDHGVPETTOSLIQFRTRDYNIRSAGPTV 1901
 Qy 242 VHCSAGVGTGPFIALDRITQQLSDSYDVAVIDLRLHRVHMQTECQVYLHOCVR 301
 Db 1902 VHCSAGVGTGPFIALDRITQQLSDSYDVAVIDLRLHRVHMQTECQVYLHOCVR 1961
 Qy 302 DVLRARKURSEQHN 315
 Db 1962 DVLRARKURSEQHN 1975

RESULT 4
 ; Sequence 2, Application US/10634027
 ; Publication No. US20040077065A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Procter & Gamble Company
 ; APPLICANT: Evdokimov, Arrem G
 ; APPLICANT: Pokross, Matthew E
 ; TITLE OF INVENTION: Three Dimensional Coordinates of HPTPbeta
 ; FILE REFERENCE: 9045M2
 ; CURRENT APPLICATION NUMBER: US/10/634,027
 ; CURRENT FILING DATE: 2003-08-04
 ; PRIOR APPLICATION NUMBER: US 60/413,547
 ; PRIOR FILING DATE: 2002-09-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO: 2
 ; LENGTH: 1997
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-634-027-2

Query Match 97.0%; Score 1691; DB 4; Length 1997;
 Best Local Similarity 99.4%; Pred. No. 3; e-152; Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DRPLSVHNLGOKGNRKTSCKPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQCDI 61
 Db 1662 DRPLSVHNLGOKGNRKTSCKPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQCDI 1721
 Qy 62 ALLPENRGKRNLYNLPYDATRKVLNSVDDPSDSDTINASYIQQNRRRTIVTQGPGLP 121
 Db 1722 ALLPENRGKRNLYNLPYDATRKVLNSVDDPSDSDTINASYIQQNRRRTIVTQGPGLP 1781
 Qy 122 TDKDPKWVQWVQVNVNITWQCVGKRCYWDQDSDVQGLP 181
 Db 1782 TDKDPKWVQWVQVNVNITWQCVGKRCYWDQDSDVQGLP 1841
 Qy 182 TIRPKKIGEOLDARLIRRHYTWPDHGVPETTOSLIQFRTRDYNIRSAGPTV 241
 Db 1842 TIRPKKIGEOLDARLIRRHYTWPDHGVPETTOSLIQFRTRDYNIRSAGPTV 1901
 Qy 242 VHCSAGVGTGPFIALDRITQQLSDSYDVAVIDLRLHRVHMQTECQVYLHOCVR 301
 Db 1902 VHCSAGVGTGPFIALDRITQQLSDSYDVAVIDLRLHRVHMQTECQVYLHOCVR 1961
 Qy 302 DVLRARKURSEQHN 315
 Db 1962 DVLRARKURSEQHN 1975

RESULT 3
 ; Sequence 3, Application US/09909567B
 ; Publication No. US20030022257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Macina, Roberto A.
 ; APPLICANT: Nai, Maoj
 ; APPLICANT: Chen, Seiru
 ; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
 ; FILE REFERENCE: DEX-014
 ; CURRENT APPLICATION NUMBER: US/09/909,567B
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 60/219,834
 ; PRIOR FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 56
 ; SEQ ID NO: 54
 ; LENGTH: 1997
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-909-567B-54

Query Match 97.0%; Score 1691; DB 4; Length 1997;
 Best Local Similarity 99.4%; Pred. No. 3; e-152; Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DRPLSVHNLGOKGNRKTSCKPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQCDI 61
 Db 1662 DRPLSVHNLGOKGNRKTSCKPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQCDI 1721
 Qy 62 ALLPENRGKRNLYNLPYDATRKVLNSVDDPSDSDTINASYIQQNRRRTIVTQGPGLP 121
 Db 1722 ALLPENRGKRNLYNLPYDATRKVLNSVDDPSDSDTINASYIQQNRRRTIVTQGPGLP 1781
 Qy 122 TDKDPKWVQWVQVNVNITWQCVGKRCYWDQDSDVQGLP 181
 Db 1782 TDKDPKWVQWVQVNVNITWQCVGKRCYWDQDSDVQGLP 1841
 Qy 182 TIRPKKIGEOLDARLIRRHYTWPDHGVPETTOSLIQFRTRDYNIRSAGPTV 241
 Db 1842 TIRPKKIGEOLDARLIRRHYTWPDHGVPETTOSLIQFRTRDYNIRSAGPTV 1901
 Qy 242 VHCSAGVGTGPFIALDRITQQLSDSYDVAVIDLRLHRVHMQTECQVYLHOCVR 301

QY 2 DRPLSVHNLGQKGRKSCPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQSDI 61
Db 1662 DRPLSVHNLGQKGRKSCPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQSDI 1721

QY 62 ALPENGRKNYNNLIPDATVKLSNVDDPSDYLASVYICNNRRTVYQGPGLG 121
Db 1722 ALPENGRKNYNNLIPDATVKLSNVDDPSDYLASVYICNNRRTVYQGPGLG 1781

QY 122 TKDDFWKQWENVNINVNTOCVEKGRYKCDYWAQDSSLYGDLQILMSSVLPW 181
Db 1782 TKDDFWKQWENVNINVNTOCVEKGRYKCDYWAQDSSLYGDLQILMSSVLPW 1841

QY 182 TIRPKIGEGBOLDARLIRHRYTWPQPHGVETOSLIQFRTRVDYINRSPGAGTV 241
Db 1842 TIRPKIGEGBOLDARLIRHRYTWPQPHGVETOSLIQFRTRVDYINRSPGAGTV 1901

QY 242 VHCSAGVGTGTFALDRILQOLDSKSDSYDVGAVDHLRHRVMOTEQVYVLHOCVR 301

Db 1902 VHCSAGVGTGTFALDRILQOLDSKSDSYDVGAVDHLRHRVMOTEQVYVLHOCVR 1961

QY 302 DVLRARKLRSQH 315
Db 1962 DVLRARKLRSQH 1975

RESULT 8

US-10-634-027-6

; Sequence 6, Application US/10634027
; Publication No. US2004077065A1
; GENERAL INFORMATION:
; APPLICANT: Procter & Gamble Company
; APPLICANT: Prokhorov, Artem G
; APPLICANT: Pokrov, Matthew E
; TITLE OF INVENTION: Three-Dimensional Coordinates of HPTbeta
; FILE REFERENCE: 9045M2
; CURRENT APPLICATION NUMBER: US/10/634,027
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/413,547
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-634-027-6

Query Match 96.9%; Score 1620; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3; 3e-153; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DRPLSVHNLGQKGRKSCPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQSDI 61
Db 1 DRPLSVHNLGQKGRKSCPIKINQPEGHFMQLQADSNLSSKEYELKDVGRNQSDI 60

QY 62 ALPENGRKNYNNLIPDATVKLSNVDDPSDYLASVYICNNRRTVYQGPGLG 121
Db 61 ALPENGRKNYNNLIPDATVKLSNVDDPSDYLASVYICNNRRTVYQGPGLG 120

QY 122 TKDDFWKQWENVNINVNTOCVEKGRYKCDYWAQDSSLYGDLQILMSSVLPW 181
Db 1264 TKDDFWKQWENVNINVNTOCVEKGRYKCDYWAQDSSLYGDLQILMSSVLPW 1323

QY 182 TIRPKIGEGBOLDARLIRHRYTWPQPHGVETOSLIQFRTRVDYINRSPGAGTV 241
Db 1224 TIRPKIGEGBOLDARLIRHRYTWPQPHGVETOSLIQFRTRVDYINRSPGAGTV 1383

QY 242 VHCSAGVGTGTFALDRILQOLDSKSDSYDVGAVDHLRHRVMOTEQVYVLHOCVR 301
Db 1384 VHCSAGVGTGTFALDRILQOLDSKSDSYDVGAVDHLRHRVMOTEQVYVLHOCVR 1443

QY 302 DVLRARK 308
Db 1444 DVLRARK 1450

RESULT 10

US-09-788-626-15

; Sequence 15, Application US/09788626
; Publication No. US2003009782A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J
; APPLICANT: Cool, Deborah E
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE

QY 181 TIRPKIGEGBOLDARLIRHRYTWPQPHGVETOSLIQFRTRVDYINRSPGAGTV 240
Db 242 VHCSAGVGTGTFALDRILQOLDSKSDSYDVGAVDHLRHRVMOTEQVYVLHOCVR 301
Db 241 VHCSAGVGTGTFALDRILQOLDSKSDSYDVGAVDHLRHRVMOTEQVYVLHOCVR 300
QY 302 DVLRARKLRSQ -313

RESULT 11
 Query Match 78.8%; Score 1374; DB 3; Length 310;
 Best Local Similarity 99.2%; Pred. No. 6 4e-123; Mismatches 0; Indels 2; Gaps 1;
 Matches 234; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 56 NOSCDALPENPENGRKRNNTLPYDATAVKLSVNDPCCSDYINASVYTPGNNPRREYV 115
 Db 1 NOSCDALPENPENGRKRNNTLPYDATAVKLSVNDPCCSDYINASVYTPGNNPRREYV 60
 QY 116 QEPFLPGEKPKDQFWKVNWNVNNTVNTVQVGRKGRVCPHWDQSDLYGQDILQMSB 175
 Db . 61 QEPFLPGEKPKDQFWKVNWNVNNTVNTVQVGRKGRVCPHWDQSDLYGQDILQMSB 120
 QY 176 SLPSTPTEPKFGEQDQHARIRRHMTWMPHGPETTOSLIQFRTRDYNRSP 235
 Db 121 SLPSTPTEPKFGEQDQHARIRRHMTWMPHGPETTOSLIQFRTRDYNRSP 178
 QY 236 GAGPTVWHSAGYGRGTPALDPLQOLDSKDSVYGAVIDLRLHRVHMVOTECQVY 295
 Db 179 GAGPTVWHSAGYGRGTPALDPLQOLDSKDSVYGAVIDLRLHRVHMVOTECQVY 238
 QY 296 LHQCVRDVLRARKLRS 311
 Db 239 LHQCVRDVLRARKLRS 254

RESULT 12
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74; Mismatches 55; Indels 3; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KISCPKINQFEGHFMQLQADSILVSLSKVEELKNGRGNNTLPENGRKRNNTL 77
 Db 20 KISKLIRVENFEAYFKQKQDNGFABEYDULKGISOPKTAELAENGRKRNNTL 1075
 QY 78 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 137
 Db 80 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 138
 QY 138 IVMVTCVEKGRVCPHWDQSDLYGQDILQMSBVFEMTIREPKGEOLDAH 197
 Db 1135 IMLTKCVOGRKTCBESWPSKO-AQDYGDTIVMTSIVLPEWTFDFTVKNTSEH 1193
 QY 198 RLIRHMTWMPHGPETTOSLIQFRTRDYNRSPGNNPRREYVQGPGRDDEKWWKBNV 257
 Db 1194 PL-RQFRTSWPQGPDTDILNFRYVLDYKQSPPESPILVHCSAGVGRGTFIA 1252
 Db 257 DRIQQDSDSKSVDYGAVHDLRLHRVHMVOTECQVYHQCVRDVLARK 308

RESULT 13
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74; Mismatches 55; Indels 3; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KISCPKINQFEGHFMQLQADSILVSLSKVEELKNGRGNNTLPENGRKRNNTL 77
 Db 1016 KISKLIRVENFEAYFKQKQDNGFABEYDULKGISOPKTAELAENGRKRNNTL 1075
 QY 78 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 137
 Db 1076 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 1134
 QY 138 IVMVTCVEKGRVCPHWDQSDLYGQDILQMSBVFEMTIREPKGEOLDAH 197
 Db 1135 IMLTKCVOGRKTCBESWPSKO-AQDYGDTIVMTSIVLPEWTFDFTVKNTSEH 1193
 QY 198 RLIRHMTWMPHGPETTOSLIQFRTRDYNRSPGNNPRREYVQGPGRDDEKWWKBNV 257
 Db 1194 PL-RQFRTSWPQGPDTDILNFRYVLDYKQSPPESPILVHCSAGVGRGTFIA 1252
 Db 258 DRIQQDSDSKSVDYGAVHDLRLHRVHMVOTECQVYHQCVRDVLARK 308

RESULT 14
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74; Mismatches 55; Indels 3; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KISCPKINQFEGHFMQLQADSILVSLSKVEELKNGRGNNTLPENGRKRNNTL 77
 Db 20 KISKLIRVENFEAYFKQKQDNGFABEYDULKGISOPKTAELAENGRKRNNTL 1075
 QY 78 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 137
 Db 80 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 138
 QY 138 IVMVTCVEKGRVCPHWDQSDLYGQDILQMSBVFEMTIREPKGEOLDAH 197
 Db 1135 IMLTKCVOGRKTCBESWPSKO-AQDYGDTIVMTSIVLPEWTFDFTVKNTSEH 1193
 QY 198 RLIRHMTWMPHGPETTOSLIQFRTRDYNRSPGNNPRREYVQGPGRDDEKWWKBNV 257
 Db 1194 PL-RQFRTSWPQGPDTDILNFRYVLDYKQSPPESPILVHCSAGVGRGTFIA 1252
 Db 258 DRIQQDSDSKSVDYGAVHDLRLHRVHMVOTECQVYHQCVRDVLARK 308

RESULT 15
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74; Mismatches 55; Indels 3; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KISCPKINQFEGHFMQLQADSILVSLSKVEELKNGRGNNTLPENGRKRNNTL 77
 Db 20 KISKLIRVENFEAYFKQKQDNGFABEYDULKGISOPKTAELAENGRKRNNTL 1075
 QY 78 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 137
 Db 80 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 138
 QY 138 IVMVTCVEKGRVCPHWDQSDLYGQDILQMSBVFEMTIREPKGEOLDAH 197
 Db 1135 IMLTKCVOGRKTCBESWPSKO-AQDYGDTIVMTSIVLPEWTFDFTVKNTSEH 1193
 QY 198 RLIRHMTWMPHGPETTOSLIQFRTRDYNRSPGNNPRREYVQGPGRDDEKWWKBNV 257
 Db 1194 PL-RQFRTSWPQGPDTDILNFRYVLDYKQSPPESPILVHCSAGVGRGTFIA 1252
 Db 258 DRIQQDSDSKSVDYGAVHDLRLHRVHMVOTECQVYHQCVRDVLARK 308

RESULT 16
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74; Mismatches 55; Indels 3; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KISCPKINQFEGHFMQLQADSILVSLSKVEELKNGRGNNTLPENGRKRNNTL 77
 Db 20 KISKLIRVENFEAYFKQKQDNGFABEYDULKGISOPKTAELAENGRKRNNTL 1075
 QY 78 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 137
 Db 80 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 138
 QY 138 IVMVTCVEKGRVCPHWDQSDLYGQDILQMSBVFEMTIREPKGEOLDAH 197
 Db 1135 IMLTKCVOGRKTCBESWPSKO-AQDYGDTIVMTSIVLPEWTFDFTVKNTSEH 1193
 QY 198 RLIRHMTWMPHGPETTOSLIQFRTRDYNRSPGNNPRREYVQGPGRDDEKWWKBNV 257
 Db 1194 PL-RQFRTSWPQGPDTDILNFRYVLDYKQSPPESPILVHCSAGVGRGTFIA 1252
 Db 258 DRIQQDSDSKSVDYGAVHDLRLHRVHMVOTECQVYHQCVRDVLARK 308

RESULT 17
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;
 Best Local Similarity 56.4%; Pred. No. 1.4e-74; Mismatches 55; Indels 3; Gaps 3;
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;
 QY 18 KISCPKINQFEGHFMQLQADSILVSLSKVEELKNGRGNNTLPENGRKRNNTL 77
 Db 20 KISKLIRVENFEAYFKQKQDNGFABEYDULKGISOPKTAELAENGRKRNNTL 1075
 QY 78 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 137
 Db 80 PYDAPTRKLSVNDPCCSDYINASVYTPGNNPRREYVQGPGRDDEKWWKBNV 138
 QY 138 IVMVTCVEKGRVCPHWDQSDLYGQDILQMSBVFEMTIREPKGEOLDAH 197
 Db 1135 IMLTKCVOGRKTCBESWPSKO-AQDYGDTIVMTSIVLPEWTFDFTVKNTSEH 1193
 QY 198 RLIRHMTWMPHGPETTOSLIQFRTRDYNRSPGNNPRREYVQGPGRDDEKWWKBNV 257
 Db 1194 PL-RQFRTSWPQGPDTDILNFRYVLDYKQSPPESPILVHCSAGVGRGTFIA 1252
 Db 258 DRIQQDSDSKSVDYGAVHDLRLHRVHMVOTECQVYHQCVRDVLARK 308

Db 1253 DRILYQIENENTDVYGVYDLEMHRPLMVPQDQVFLNQCVLDIVRSOK 1303

RESULT 13

; Sequence 42, Application US/10366547

; Publication No. US20030215891A1

; GENERAL INFORMATION:

; APPLICANT: Meng, Tau-Ching

; APPLICANT: Toks, Nicholas K.

; APPLICANT: Cool, Deborah E.

; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE

; FILE REFERENCE: 200125 439

; CURRENT APPLICATION NUMBER: US/10/366,547

; CURRENT FILING DATE: 2003-02-12

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 42

; LENGTH: 1337

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-366-547-42

Query Match 50.4%; Score 878 5; DB 4; Length 1337; Best Local Similarity 56.4%; Pred. No. 1.e-74; Mismatches 68; Indels 3; Gaps 3; Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

Qy 18 KTSCKPIKINQFEGHFMKLOADSNSYLSSKEYELDKVERNOSCDIALPENRGKRYNNIL 77

Db 1016 KUSKLIRVENFAFKQKODNSGPAEEVEDIKLUVISQPKYAAELAENGKRYNNIL 1075

Qy 78 PYDATRVSUKNYDDPDCSYINASYFGNNFRBEYVTOQPLGKTPKODPFLKDFWVNMEKNTYA 137

Db 1016 KUSKLIRVENFAFKQKODNSGPAEEVEDIKLUVISQPKYAAELAENGKRYNNIL 1075

Qy 78 PYDATRVSUKNYDDPDCSYINASYFGNNFRBEYVTOQPLGKTPKODPFLKDFWVNMEKNTYA 137

Db 1076 PYDISRVSU-S-YOTHSSTDINANMHEGHSKQFIATQPLGKTPKODPFLKDFWVNMEKNTYA 1134

Qy 138 IWMTOCVERKGRVKCQHYPADDSLYGDLIQLQMSSESVPENMIREPKCIGEBOLOAH 197

Db 1135 IMLTKCVOGRKTCSEYIPSKQ-AQDYGITVAMSETVLPENMIREPKCIGEBOLOAH 1193

Qy 198 RLIRPHFVWPDHGVPETOSLIQFRTVDRYINSPGAGPTVHCSAGYGRGTFIAL 257

Db 1194 PL-RQFHFTSWPDHGVPDFTDLINFLRUDTMKQSPSPSPILVHCSAGYGRGTFIAL 1252

Qy 258 DRILQIENENTDVYGVYDLEMHRPLMVPQDQVFLNQCVLDIVRSOK 308

Db 1135 IMLTKCVOGRKTCSEYIPSKQ-AQDYGITVAMSETVLPENMIREPKCIGEBOLOAH 197

Qy 138 IWMTOCVERKGRVKCQHYPADDSLYGDLIQLQMSSESVPENMIREPKCIGEBOLOAH 197

Db 1135 IMLTKCVOGRKTCSEYIPSKQ-AQDYGITVAMSETVLPENMIREPKCIGEBOLOAH 1193

Qy 198 RLIRPHFVWPDHGVPETOSLIQFRTVDRYINSPGAGPTVHCSAGYGRGTFIAL 257

Db 1194 PL-RQFHFTSWPDHGVPDFTDLINFLRUDTMKQSPSPSPILVHCSAGYGRGTFIAL 1252

Qy 258 DRILQIENENTDVYGVYDLEMHRPLMVPQDQVFLNQCVLDIVRSOK 308

Db 1253 DRILYQIENENTDVYGVYDLEMHRPLMVPQDQVFLNQCVLDIVRSOK 1303

RESULT 15

; Sequence 2, Application US/10723606

; Publication No. US20040161821A1

; GENERAL INFORMATION:

; APPLICANT: Palka-Hamblin, Helena L.

; APPLICANT: Toks, Nicholas K.

; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE

; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS

; TITLE OF INVENTION: AND RELATED METHODS

; FILE REFERENCE: 200125 447

; CURRENT APPLICATION NUMBER: US/10/723,606

; CURRENT FILING DATE: 2003-11-26

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2

; LENGTH: 1337

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-723-606-2

Query Match 50.4%; Score 878 5; DB 4; Length 1337; Best Local Similarity 56.4%; Pred. No. 1.e-74; Mismatches 68; Indels 3; Gaps 3; Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

Qy 18 KTSCKPIKINQFEGHFMKLOADSNSYLSSKEYELDKVERNOSCDIALPENRGKRYNNIL 77

Db 1016 KUSKLIRVENFAFKQKODNSGPAEEVEDIKLUVISQPKYAAELAENGKRYNNIL 1075

Qy 78 PYDATRVSUKNYDDPDCSYINASYFGNNFRBEYVTOQPLGKTPKODPFLKDFWVNMEKNTYA 137

Db 1076 PYDISRVSU-S-YOTHSSTDINANMHEGHSKQFIATQPLGKTPKODPFLKDFWVNMEKNTYA 1134

Qy 138 IWMTOCVERKGRVKCQHYPADDSLYGDLIQLQMSSESVPENMIREPKCIGEBOLOAH 197

Db 1135 IMLTKCVOGRKTCSEYIPSKQ-AQDYGITVAMSETVLPENMIREPKCIGEBOLOAH 1193

Qy 198 RLIRPHFVWPDHGVPETOSLIQFRTVDRYINSPGAGPTVHCSAGYGRGTFIAL 257

Db 1194 PL-RQFHFTSWPDHGVPDFTDLINFLRUDTMKQSPSPSPILVHCSAGYGRGTFIAL 1252

Qy 258 DRILQIENENTDVYGVYDLEMHRPLMVPQDQVFLNQCVLDIVRSOK 308

Db 1253 DRILYQIENENTDVYGVYDLEMHRPLMVPQDQVFLNQCVLDIVRSOK 1303

Search completed: February 17, 2006, 01:39:43

Query Match Similarity 50.4%; Score 878.5; DB 4; Length 1337;

Best Local Similarity 56.4%; Pred. No. 1.e-74; Length 1337;

US-10-366-547-44

PRIOR APPLICATION NUMBER: 60/584,405
 PRIORITY FILING DATE: 2004-06-30
 NUMBER OF SEQ ID NOS: 527
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 1445
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-169-041-181

Query Match 35.3%; Score 616.5; DB 7; Length 1445;
 Best Local Similarity 37.8%; Pred. No. 1.2e+49; Mismatches 106; Indels 49; Gaps 8;
 Matches 133; Conservative

Qy 12 GOKGNRK-----TSCP-----KINOPFCHPMQLQDSDNY 41
 Db 787 GEGRSRKCFOTAHYFVVEDSSSPRVPNNEISIPIPFPDMEALPVKOFVHGELYNSNQ 846

Qy 42 LSKKEYERLK--DYGRRNQSCDIALPENRGKRNNTLYDTRVLSNV--DDDCSDY 97
 Db 847 GSEDEDEBVRCTADMITEEHSHEPMKHONRYNLLAIDSYRVLRIPEKSDHSDY 906

Qy 98 INASYIFGNFRPRYIVTQGSLPJKDDFKWKNWQVNENIVWTCVAKGRVRCYHWP 157
 Db 907 INANYTGDYGNKAKAYIATQSPKTSFEDFWRMWIMWQNTGIVWNTLVKGRRKCDQWQ 966

Qy 158 AQQDLSXQGLLQMLSESVLPEMTRPKKGEQQLDA-----HRLIRPHHYW 207
 Db 967 T-ENSEBVGNIIVTLYKSTKTHACTVTRFSTRNTVKKQKQKPNKPRONERVWQHYZQ 1025

Qy 208 WPDHGVPETQTSIQLQFVTRVYDYNIRSPGAGPVTWCSAGVGRTEPFLDRILQDLSK 267
 Db 1026 WPDHGVPETALVPLTFVR--RSSAARMETGPVVLHCSAGVGRGTYIVDLSWQKOK 1083

Qy 268 DSDVDTYGAVIDLULHRVYMQTPEOYVLYHOCVVRVL--RARKLSEQHHH 317
 Db 1084 STVNVLGPKLKHITQRNVLVQTEOYVIFPFDALLAIGKETEVSSNQHSHY 1135

RESULT 11
 US-10-821-234-1102
 Sequence 1102, Application US/10821234
 Publication No. US2005025514A1
 GENERAL INFORMATION
 APPLICANT: Labach, Ivan
 APPLICANT: Stabach-Crain, Birgit
 APPLICANT: Andramani, Susan
 APPLICANT: Tang, Y-Tom
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 FILE REFERENCE: 821A
 CURRENT APPLICATION NUMBER: US/10-821,234
 CURRENT FILING DATE: 2004-04-07
 PRIOR APPLICATION NUMBER: US 60/462,047
 PRIOR FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 1704
 SOFTWARE: pt-SEQ_genes Version 1.0
 SEQ ID NO: 1102
 LENGTH: 1452
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match 35.0%; Score 610; DB 6; Length 1452;
 Best Local Similarity 44.6%; Pred. No. 5.1e+49; Mismatches 103; Indels 10; Gaps 5;
 Matches 125; Conservative 42; Mismatches 103; Indels 10; Gaps 5;

Qy 23 IKNOPGEHFMQLQDSDNYNLSKEYERLKQVGRNQSCDIALPENRGKRNNTLYPDA 81
 Db 880 IRYVADLGHITQMKCAEGYGFKEYSSFFS-GQSAQWDSAKDENTMENRGNNTAYHQS 938

Qy 82 TRVKLSNVDDPESDYINASYIFGNFRREVIVTQGPLGPTKDDFWRMWIMWQNVHIVWY 141
 Db 130 SRYVLTISIVPESDYINANYDGYRKONAYATQGPETGDFWRYMWEQRTAVMM 189

Qy 22 PIKNOPEHFMQLQDSDNYNLSKEYERLKQVGRNQSCDIALPENRGKRNNTLYPDA 81
 Db 71 PIPDIDLMANIEIHLKANDGKFSSEYI-DPGDOFTWENSLNEYENPKPDRYANVYD 129

Qy 82 TRVKLSNVDDPESDYINASYIFGNFRREVIVTQGPLGPTKDDFWRMWIMWQNVHIVWY 141
 Db 130 SRYVLTISIVPESDYINANYDGYRKONAYATQGPETGDFWRYMWEQRTAVMM 189

Qy 142 TOCVERGKRCYDPMYWDPSLQYDQTLQNSLSSVPEMTREKL--CGEQLDAHL 199
 Db 190 TRLEEKSRVKCDOYIWPW-RGTFETGQIQLQVFLDVTVELATYVTRIPALHKGSGSE--KRE 245

Qy 200 IRHRYTYWMDHGVPETQTSIQLQFVTRVYDYNIRSP-GAGPVTWCSAGVGRGTYW 258

RESULT 13
 US-10-821-234-1635
 ; Sequence 1635, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Sacha-Crain, Birgit
 ; APPLICANT: Andramani, Susan
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821-234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIORITY APPLICATION NUMBER: US 60/462,047
 ; PRIORITY FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: PRSEQ_genes version 1.0
 ; SEQ ID NO: 1635
 ; LENGTH: 1897
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ;
 ; Query Match 33.5%; Score 586; DB 6; Length 1897;
 ; Best Local Similarity 42.6%; Pred. No. 1.3e-46;
 ; Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;
 ;
 ; Query 22 PIKINQPECHFWMQLADSNVLSKEEELKDVGNPQCDIALLENGKRNQYNTLPDA 81
 ; Db 1321 PIPIBLADNIBERKLANDGKLFQSEYESI-DPGQQFTWENSLENKPNRKNYANVAYDH 1379
 ; Qy 82 TRVKLSNVNDPDSYDINASYIIGYRKQNAVIAQGELPGRKDPFWKQWVNQVNTIVN 141
 ; Db 1380 SRVILTSIDGVGSDYDINASYIIGYRKQNAVIAQGELPGRKDPFWKQWVNQVNTIVN 1439
 ; Qy 142 TOCVERGKGRVCDYIWADDSLYGDLILOMSBSVPEWTFREKLI-CGEBOLDAHL 199
 ; Db 1440 TRLEBSRKRKDQYWA-RGTERGQIQLQVILDVEELATYVTFALHKGSSSE--KRE 1495
 ;
 ; Query Match 33.5%; Score 586; DB 7; Length 1907;
 ; Best Local Similarity 42.6%; Pred. No. 1.3e-46;
 ; Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;
 ;
 ; Query 22 PIKINQPECHFWMQLADSNVLSKEEELKDVGNPQCDIALLENGKRNQYNTLPDA 81
 ; Db 1331 PIPIBLADNIBERKLANDGKLFQSEYESI-DPGQQFTWENSLENKPNRKNYANVAYDH 1389
 ; Qy 82 TRVKLSNVNDPDSYDINASYIIGYRKQNAVIAQGELPGRKDPFWKQWVNQVNTIVN 141
 ; Db 1390 SRVILTSIDGVGSDYDINASYIIGYRKQNAVIAQGELPGRKDPFWKQWVNQVNTIVN 1449
 ; Qy 142 TOCVERGKGRVCDYIWADDSLYGDLILOMSBSVPEWTFREKLI-CGEBOLDAHL 199
 ; Db 1450 TRLEBSRKRKDQYWA-RGTERGQIQLQVILDVEELATYVTFALHKGSSSE--KRE 1505
 ;
 ; Query Match 33.5%; Score 586; DB 7; Length 1907;
 ; Best Local Similarity 42.6%; Pred. No. 1.3e-46;
 ; Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;
 ;
 ; Query 22 PIKINQPECHFWMQLADSNVLSKEEELKDVGNPQCDIALLENGKRNQYNTLPDA 81
 ; Db 1331 PIPIBLADNIBERKLANDGKLFQSEYESI-DPGQQFTWENSLENKPNRKNYANVAYDH 1389
 ; Qy 82 TRVKLSNVNDPDSYDINASYIIGYRKQNAVIAQGELPGRKDPFWKQWVNQVNTIVN 141
 ; Db 1390 SRVILTSIDGVGSDYDINASYIIGYRKQNAVIAQGELPGRKDPFWKQWVNQVNTIVN 1449
 ; Qy 142 TOCVERGKGRVCDYIWADDSLYGDLILOMSBSVPEWTFREKLI-CGEBOLDAHL 199
 ; Db 1506 LRQFQMPAWPDHGVPYPTPLAFRVRKAC--NPLDAGMVWHCSAGVGRGTCFIVD 1562
 ; Qy 1496 LRQFQMPAWPDHGVPYPTPLAFRVRKAC--NPLDAGMVWHCSAGVGRGTCFIVD 1552
 ;
 ; Query Match 33.5%; Score 586; DB 7; Length 1907;
 ; Best Local Similarity 42.6%; Pred. No. 1.3e-46;
 ; Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;
 ;
 ; Query 22 PIKINQPECHFWMQLADSNVLSKEEELKDVGNPQCDIALLENGKRNQYNTLPDA 81
 ; Db 1563 AMLERKHKHKTVDIYHVNMRQSNYMWQEDOYVTHEALLEATCGHTEVPARNL 1620
 ;
 ; RESULT 14
 ; US-11-000-463-250
 ; Sequence 250, Application US/11000463
 ; Publication No. US200506643A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Weinman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Cao, Yi-Cheng
 ; APPLICANT: Dumanac, Radjoje T.
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 ;
 ; RESULT 15
 ; US-10-528-031-47
 ; Sequence 47, Application US/10528031
 ; Publication No. US200506257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OXIDS BIOMED Forschungs- und Entwicklungs GmbH
 ; APPLICANT: Guell, Christian
 ; APPLICANT: Buck, Charles R.
 ; TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for
 ; title of invention: prevention, diagnosis or treatment of liver disorders and epi-
 ; FILE REFERENCE: Orlis Biomed, A031
 ; CURRENT APPLICATION NUMBER: US/10/528,031
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 47
 ; LENGTH: 1254
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ;
 ; Query Match 33.5%; Score 583.5; DB 6; Length 1254;
 ;
 ; Query Match 33.5%; Score 583.5; DB 6; Length 1254;

KW	immunomodulator; gene therapy; metabolic disease; eating disorders;
KW	body-weight regulation disorder; cachexia; diabetes mellitus; cancer;
KW	hypertension; coronary heart disease; hypercholesterolaemia; gallstone;
KW	dyslipidaemia; osteoarthritis; sleep apnea; human; chromosome 12;
KW	protein tyrosine phosphatase receptor type B precursor; PTPrB.
XX	<i>Homo sapiens.</i>
XX	WO2003047611-A2.
XX	12-JUN-2003.
PD	04-DEC-2002; 2002WO-EP013744.
PR	04-DEC-2001; 2001EP-00128844.
PR	07-DEC-2001; 2001EP-00128138.
PR	02-JAN-2002; 2002EP-00000010.
XX	(DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX	Meuse M, Bulenbergs K, Fritsch R, Haeder T, Brenner G;
PI	Steuerriegel A;
XX	WPI; 2003-532801/50.
DR	DR-N-PSDB; ACC79776.
XX	New compositions comprising tyrosine phosphatase genes or proteins useful for treating or preventing metabolic diseases, e.g. as obesity or cachexia.
PS	Claim 2; FIG. 8B; 83pp; English.
PT	The present invention describes a pharmaceutical composition comprising a kinase Tec or egg-derived tyrosine phosphatase PTPrB, non-receptor protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene for treating or preventing metabolic diseases, e.g. as obesity or cachexia.
XX	The present invention describes a pharmaceutical composition comprising a nucleic acid (1) protein tyrosine phosphatase PTPrB, non-receptor protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene family or encoded polypeptide, fragment or variant of nucleic acid molecule or polypeptide, an antibody, an aptamer or receptor recognising a nucleic acid molecule of PTPrB, Tec, or EDTP gene family or encoded polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical composition can have antidiabetic, hypotensive, cardiotonic, antihypertensive, osteopathic, cytostatic, anorectic and immunomodulator activities, and can be used in gene therapy. The composition is useful for the manufacture of an agent for detecting and/or verifying, for treating and alleviating and/or preventing a disorder, including metabolic diseases such as obesity and other body weight regulation disorders, as well as related disorders such as eating disorder, cachexia, diabetes mellitus, hypertension, coronary heart disease, hypercholesterolaemia, osteoarthritis, dyslipidaemia, osteoarthritis, galactose, cancers (cancers of the reproductive organ), sleep apnea, and other diseases, in cells, cell masses, organs and/or subjects. The components of the composition may also be used in controlling the function of a gene and/or gene product which is influenced and/or modified by a PTPrB, Tec, or EDTP homologous polypeptide, and for identifying substances capable of interacting with a PTPrB, Tec or EDTP homologous polypeptide. The nucleic acid molecule of PTPrB, Tec, or EDTP family or their fragments may be used in the preparation of a non-human animal which over- or under-expresses the PTPrB, Tec, or EDTP gene product. The present sequence represents human protein tyrosine phosphatase receptor type B precursor (PTPrB), which is a human PTPrB homologous sequence. Human PTPrB is located to chromosome 12.
SQ	Sequence 1997 AA;
Query Match	97.0%; Score 1691; DB 7; Length 1997;
Best Local Similarity	99.4%; Pred. No. S.60-179;
Matches	312; Conservative 1; Mismatchs 1; Indels 0; Gaps 0;
Qy	2 DRPLSVHLNLGOKGNKRTSPKINQAFEGHFMQQLADSNTVLSKVEELKQVGRNQCDI 61
Db	1662 DRPLSVHLNLGOKGNKRTSPKINQAFEGHFMQQLADSNTVLSKVEELKQVGRNQCDI 1721
Oy	62 ALLPENRGRKGRNINLPIYDTRIVLNSVDDPCSYINASITPGNFRREVYVQGPIG 121
RESULT 7	ADD70329
ID	ADD70329 standard; protein; 1997 AA.
XX	AC ADD70329;
XX	DT 06-MAY-2004 (first entry)
XX	DE Human heat mitochondrial protein as a therapeutic target SeqIDB2135.
XX	XX
XX	KW mitochondrial; human; screening assay; diabetes mellitus;
XX	KW Huntington's disease; osteoarthritis;
XX	KW Leber's hereditary optic neuropathy; ITHON;
XX	KW mitochondrial encephalopathy; lactic acidosis and stroke; MELAS;
XX	KW myoclonic epilepsy; ragged red fire syndrome; MERRF; cancer;
XX	KW neuroprotective; notropic; antidiabetic; anticonvulsant; antiarthritic;
XX	KW osteopathic; ophthalmological; cytostatic.
CC	<i>Homo sapiens.</i>
CC	XX
CC	WO2003087768-A2.
CC	PD 23-OCT-2003.
CC	XX
CC	PF 04-APR-2003; 2003WO-US010870.
CC	XX
CC	PR 12-APR-2002; 2002US-0312843P.
CC	PR 17-JUN-2002; 2002US-0319987P.
CC	PR 20-SEP-2002; 2002US-0412418P.
CC	XX
CC	PA (MITO-) MITKOR.
CC	PA (BUCK-) BUCK INST AGE FES.
CC	XX
CC	PI Ghosh SS, Raby ED, Zhang B, Gibson BW, Taylor SW, Gleam GM;
CC	PI Wernock DE;
CC	XX
CC	WPI; 2003-845369/78.
CC	XX
CC	PT Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, PT comprises detecting a modified polypeptide in a sample and correlating PT with the disease.
CC	XX
CC	Claim 1; SEQ ID NO 2135; 180pp; English.
PS	XX
PS	This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease,

XX 05-FEB-2001; 2000US-004698. PR 03-FEB-2000; 2000US-004694. PR 27-APR-2000; 2000US-0056075. PR 19-JUL-2000; 2000US-0062025. PR 01-SEP-2000; 2000US-00661561. PR 20-OCT-2000; 2000US-0069325. PR 30-NOV-2000; 2000US-00728422. PR (HYSF-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; PI Xue AJ, Yang Y, Wejhrman T, Goodrich R; DR WPI; 2001-476283/51. DR N-FSDB; AAKS2938.

XX PR Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy. PT XX PS Claim 20; Page 340-341; 6221pp; English.

XX CC The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAKS1456-AAKS3435) that exhibit activity eliciting cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, 'vaccines' or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAKS020) are omitted as the relevant Pages from the sequence listing were missing at the time of publication

XX SQ Sequence 2002 AA;

XX Query Match 97.0%; Score 1691; DB 4; Length 2002; Best Local Similarity 99.4%; Pred. No. 5.6e-179; Matches 312; Conservative 1; Indels 0; Gaps 0; CC

CC 2 DRPLSVLNLQGQKAKRKTSCIKINQPFCHFMQLQADSNTLUSKEYELKVGVRNQSDI 61

CC 1667 DRPLSVLNLQGQKAKRKTSCIKINQPFCHFMQLQADSNTLUSKEYELKVGVRNQSDI 1726

CC 62 ALPPENRKGKRYNNILPVDATRVKLUSNVDDPCSDYINASVYIENRREYIVTOGPPLG 121

CC 1727 ALPPENRKGKRYNNILPVDATRVKLUSNVDDPCSDYINASVYIENRREYIVTOGPPLG 1786

CC 122 TQDPPWMMWQHQHNNWVTOCUEKGKVKHWWADDSQIYGDLLQQLSSVDE 181

CC 1787 TQDPPWMMWQHQHNNWVTOCUEKGKVKHWWADDSQIYGDLLQQLSSVDE 1846

CC 182 TIREFCKCGBQDAAHLIRLIRHPTYWDHGPGPETOQSIQFRTVDYINRSGAGTV 241

CC 1847 TIREFCKCGBQDAAHLIRLIRHPTYWDHGPGPETOQSIQFRTVDYINRSGAGTV 1906

CC 242 VHCASGAGTGTFALDRIQQQLSKSDWYGAVIDLRLRHPTYWDHGPGPETOQSIQFRTVDYINRSGAGTV 301

CC 1907 VHCASGAGTGTFALDRIQQQLSKSDWYGAVIDLRLRHPTYWDHGPGPETOQSIQFRTVDYINRSGAGTV 1966

CC 302 DYLARKLSEOHH 315

CC 1967 DYLARKLSEOHH 1980

XX SQ Sequence 312 AA;

XX Query Match 95.9%; Score 1590; DB 8; Length 312; Best Local Similarity 100.0%; Pred. No. 3.9e-180; Matches 312; Conservative 0; Indels 0; Gaps 0; CC

CC 2 DRPLSVLNLQGQKAKRKTSCIKINQPFCHFMQLQADSNTLUSKEYELKVGVRNQSDI 61

CC 1 DRPLSVLNLQGQKAKRKTSCIKINQPFCHFMQLQADSNTLUSKEYELKVGVRNQSDI 60

CC 62 ALPPENRKGKRYNNILPVDATRVKLUSNVDDPCSDYINASVYIENRREYIVTOGPPLG 121

CC 61 ALPPENRKGKRYNNILPVDATRVKLUSNVDDPCSDYINASVYIENRREYIVTOGPPLG 120

CC 122 TQDPPWMMWQHQHNNWVTOCUEKGKVKHWWADDSQIYGDLLQQLSSVDE 181

CC 121 TQDPPWMMWQHQHNNWVTOCUEKGKVKHWWADDSQIYGDLLQQLSSVDE 180

CC 182 TIREFCKCGBQDAAHLIRLIRHPTYWDHGPGPETOQSIQFRTVDYINRSGAGTV 241

OS Homo Sapiens.

OS Synthetic.

PN US2004077065-A1.

XX PD 22-AFP-2004.

XX PF 04-AUG-2003; 2003US-00634027.

XX PR 25-SEP-2002; 2002US-0413547P.

XX PA (PROC) PROCTER & GAMBLE CO.

XX PI Evdokimov AG, Pokross ME;

XX DR WPI; 2004-374235/35.

XX DR N-PSB; ADO04583.

XX PT Identification of compound useful for treatment of angiogenesis mediated disorder, by using three-dimensional structure of HPrpbeta catalytic domain, and employing structure to design, or select compound that binds HPrpbeta in silico.

XX PT Disclosure; SEQ ID NO 6; 335pp; English.

XX CC The invention relates to the three dimensional coordinates of HPrpbeta (also known as HPrp-beta, PPrp, PPrpeta, PPrp or R-Prp-beta) protein. It also relates to a method for the identification of a compound useful for the treatment of an angiogenesis mediated disorder. The compounds identified by this method are useful to treat disease like diabetic retinopathy, sickle cell anaemia, Paget's disease, mycobacterial infections, systemic lupus erythematosus, myopia, Crohn's disease, psoriasis, rheumatoid arthritis, solid or blood borne tumours and acquired immune deficiency syndrome (AIDS). The invention is useful for the treatment of an angiogenesis mediated disorder or disease. It is also useful in drug design techniques. The present sequence is human HPrpbeta intracellular domain (ICD) truncated protein.

XX SQ Sequence 312 AA;

XX Query Match 100.0%; Score 1590; DB 8; Length 312; Best Local Similarity 100.0%; Pred. No. 3.9e-180; Matches 312; Conservative 0; Indels 0; Gaps 0; CC

CC 2 DRPLSVLNLQGQKAKRKTSCIKINQPFCHFMQLQADSNTLUSKEYELKVGVRNQSDI 61

CC 1 DRPLSVLNLQGQKAKRKTSCIKINQPFCHFMQLQADSNTLUSKEYELKVGVRNQSDI 60

CC 62 ALPPENRKGKRYNNILPVDATRVKLUSNVDDPCSDYINASVYIENRREYIVTOGPPLG 121

CC 61 ALPPENRKGKRYNNILPVDATRVKLUSNVDDPCSDYINASVYIENRREYIVTOGPPLG 120

CC 122 TQDPPWMMWQHQHNNWVTOCUEKGKVKHWWADDSQIYGDLLQQLSSVDE 181

CC 121 TQDPPWMMWQHQHNNWVTOCUEKGKVKHWWADDSQIYGDLLQQLSSVDE 180

CC 182 TIREFCKCGBQDAAHLIRLIRHPTYWDHGPGPETOQSIQFRTVDYINRSGAGTV 241

Db 1194 PL-ROPHFTSWFDHSUPFTDALLINERFLYDVKQSPPSPLVHQSAGUGRGTFLI 1252
 Qy 258 DRILYQIENENTVYDGYIVLPLRMLPMLVQTEQVFLNQCVLUDIRSOK 308
 Db 1253 DRILYQIENENTVYDGYIVLPLRMLPMLVQTEQVFLNQCVLUDIRSOK 1303

RESULT 4

HPP betta-like tyrosine phosphatase precursor - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 15-Feb-1999 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S68700

R;Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Saioh, T.; Ohnugi, M.; Yamamoto, T.
 FEBs Lett. 378: 7-14, 1995
 A;Title: Molecular cloning and characterization of BYP, a murine receptor-type tyrosine kinase. Molecular cloning and characterization of BYP, a murine receptor-type tyrosine kinase.
 A;RefSeq: S68700
 A;Accession: S68700
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 11238 <XOR>
 A;Cross-references: UNIPROT:064455; UNIPARC:UPI0000013C2; GB:D45212; NID:91208432; PIDN:68700
 C;Genetics:
 C;genetics:
 C;superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repeat
 C;Keywords: phosphoprotein
 C;Keywords: phosphoprotein
 C;Keywords: protein sequence #status predicted <S>
 P;9-1238/Product: HPP betta-like tyrosine phosphatase #status predicted <MAT>
 P;9-1238/Domain: fibronectin type III repeat homology <PR>
 P;966-188/Domain: protein-tyrosine phosphatase homology <PR>
 F;1140/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1146/Binding site: substrate phosphate (Arg) #status predicted

Query Match 48.6%; Score 847.5; DB 2; Length 1557;
 Best Local Similarity 55.6%; Pred. No. 1.7e-64; Matches 160; Conservative 45; Gaps 7; Indels 3; Mismatches 76; Codon 3; PIDN:68700

Db 1250 PLIKONFAHYRIMSDSPRSFSEELKVKRSDQCTFDLPCNPKPTNLPH 1309

Qy 82 PPIKINQFEEHFMKQLDSDNLFLSKEYVELDKDVSERNQSCDALLPENRGRKRYNLPIDA 81

Db 1310 SRFKLPQVUDDGSDSYDINANVYFGHSNPREFTVQGPIHSTRDPWRMCWSN 1369

Qy 142 TCOVEKGRKRDHYMPADDSLYQDGLIQLMSESLVPEWTRPKIC-GBQDABRHLI 200

Db 1370 TPIEPEKGRKRDHYMPADDSLYQDGLIQLMSESLVPEWTRPKIC-GBQDABRHLI 1425

Db 1426 RHFHTFTWDFGVNPNPQTLVRFVRAFRDL--CAEORPIVHCSAGGRSOTFTLDR 1483

Qy 261 LOQUSKSDVDYGAHDRLRHLVHMQTYCQVYLYHOCVDVARK 308

Db 1484 LOQINNSDVKDIFGIVYAMKERVWVQVQYICHOCLLAVALRGKE 1531

RESULT 5

D4214 IVMVTOCUEKGRKRDHYMPADDSLYQDGLIQLMSESLVPEWTRPKICGSEQLDAH 197

Db 1036 IVMTCVKEQGRKRDHYMPADDSLYQDGLIQLMSESLVPEWTRPKICGSEQLDAH 1094

Qy 198 RLIGHFHTFTWDFGVNPNPQTLVRFVRAFRDL--CAEORPIVHCSAGGRSOTFTLDR 257

Db 1095 PL-ROPHFTSWFDHSUPFTDALLINERFLYDVKQSPPSPLVHQSAGUGRGTFLI 1153

Qy 258 DRILYQIENENTVYDGYIVLPLRMLPMLVQTEQVFLNQCVLUDIRSOK 308

Db 1154 DRILYQIENENTVYDGYIVLPLRMLPMLVQTEQVFLNQCVLUDIRSOK 1204

RESULT 5

D4214 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, short splice form precursor

C;Species: Drosophila melanogaster
 C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
 C;Accession: D4214
 C;Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sub

R;Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W.
 Celi 67, 661-673, 1991
 A;Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sub
 A;Reference number: A4214; MUID:92034988; PMID:1657401
 A;Accession: C4214
 A;Molecule type: mRNA
 A;Residues: 1-1630 <XAN>
 A;Cross-references: UNIPROT:UPI0000177054; GB:W80465
 C;Genetics:
 C;Gene: FlyBase:Pt10D
 C;Cross-references: FlyBase:FBgn0004370
 C;Superfamily: protein-tyrosine phosphatase, receptor type 4E; fibronectin type III repeat
 C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor
 F;1214-1213/Domain: transmembrane #status predicted <TM>
 F;1205-1515/Domain: intracellular #status predicted <IN>
 F;1467/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1474/Binding site: substrate phosphate (Arg) #status predicted

Query Match 48.6%; Score 847.5; DB 2; Length 1630;
 Best Local Similarity 55.6%; Pred. No. 1.7e-64; Matches 160; Conservative 45; Mismatches 76; Indels 7; Gaps 3; PIDN:68700

F;30-819/Domain: extracellular #status predicted <EXT>
 F;31-115/Domain: fibronectin type III repeat homology #status atypical <FN3>
 F;316-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>
 F;411-415/Domain: fibronectin type III repeat homology <FN4>
 F;431-519/Domain: fibronectin type III repeat homology <FN5>
 F;58-625/Domain: fibronectin type III repeat homology <FN6>
 F;620-713/Domain: fibronectin type III repeat homology <FN7>
 F;721-810/Domain: fibronectin type III repeat homology <FN8>
 F;811-875-876-1187/Domain: protein tyrosine phosphatase phi, long form #status predicted <PTP1>
 F;819-843/Domain: protein tyrosine phosphatase phi, short form #status predicted <PTP2>
 F;844-1187/Domain: intracellular #status predicted <INT>
 F;901-1187/Domain: protein tyrosine phosphatase phi, cytosolic form #status predicted <PTP3>
 F;923-1155/Domain: protein tyrosine phosphatase homology <PTP4>
 F;925-14-119-201-227-286-323-369-460-489-699-711-732-789/Binding site: carbohydrate
 F;107/Active site: Cys (phosphocysteine intermediate) #status predicted <PTP5>
 F;1113/Binding site: substrate phosphate (Arg) #status predicted <PTP6>

Query Match 43.6%; Score 760.5; DB 1; Length 1187;
 Best Local Similarity 49.8%; Pred. No. 3.e-57; Mismatches 81; Indels 7; Gaps 3;
 Matches 143; Conservative 56; Mismatches 81; Indels 7; Gaps 3;

Query 17 RKTCPKINQFEGHMKQADANSYILKSKYEELKGRNQSCDIALPENRGKRYNN 76
 Db 883 RKLTPVQVOLDEDDAYKVKDQAKSDQYKPSLQFELKLIGDIPHRADQPLRCKORYNN 942

Query 77 LPYDPIRTRKLSDVDDPDCSDYINASVYGNFRAYVTOCPLGKTDKDFKMMWQOMH 136
 Db 943 LPYDPIRTRKLSDVDDPDCSDYINASVYGNFRAYVTOCPLGKTDKDFKMMWQOMH 1002

Query 137 NIYVMTQCEVKGRVKCDHWPADQDSLYKQDILQMLMSESTUPWTFKICGHEOLDA 196
 Db 1003 MIVMUDTOCNEKERVKCDHWPFTBEPVAGDITVEMSEBODDWAHRHFRI--NYADE 1059

Query 197 HRLTRHFTYTWPDIGKPV--ETTOSLQIYFRTVDYINRSPGAGTVHCCAGVORTSF 254
 Db 1060 MQDWHFPTVAPDQHGPVPAALESTQFHMROQATK--KPMTHCAGVORTTF 1117

Query 255 IALRILQDQSKDSVUDVYGAVIDLHLRHRVHVMVOTECQVYVILHOCR 301
 Db 1118 IALRILQDQSKDSVUDVYGAVIDLHLRHRVHVMVOTECQVYVILHOCR 1164

RESULT 15

A49724 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
 N: Alternative names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SAP-1;
 C: Species: Homo sapiens (man);
 C: Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C: Accession: A49724
 C: Matosaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.; Biol. Chem. 269, 2075-2081, 1994
 A: Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase and
 A: Reference number: A49724; MUID:94124551; PMID:8224459
 A: Accession: A49724
 A: Molecule type: mRNA
 A: Residues: 1-1118 <MTO>
 C: Cross-references: UNIPROT:Q15426; UNIPARC:UPI0000073BP2; GB:D15049; NID:9475003; PIDN:
 C: Gene: GDR; PTTRH; SAP-1
 A: Cross-references: GDR:005504
 A: Map position: 19q13.4-19q13.4
 A: Note: highly expressed in colon and pancreatic cancer cells but not in the normal cell
 C: Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repeat
 C: Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric monoester
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;27-110/Domain: fibronectin type III repeat homology <3FNA>
 F;88-118/Domain: protein tyrosine phosphatase, receptor type H #status predicted <MAT>
 F;188-711/Domain: extracellular #status predicted <EXT>
 F;116-999/Domain: fibronectin type III repeat homology <3FNB>
 F;296-389/Domain: fibronectin type III repeat homology <3FNC>
 F;385-468/Domain: fibronectin type III repeat homology <3FNE>

F;474-558/Domain: fibronectin type III repeat homology <3FNE>
 F;564-655/Domain: fibronectin type III repeat homology <3FNE>
 F;567-737/Domain: fibronectin type III repeat homology <3FNE>
 F;662-778/Domain: transmembrane #status predicted <TM>
 F;779-1118/Domain: intracellular #status predicted <INT>
 F;94-107/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;155-79-83-107-132-149-172-196-203-286-306-312-329-352-376-383-401-436-439-470-490-558
 F;1022/Active site: Cys (phosphocysteine intermediate) #status predicted <PTP2>
 F;1028/Binding site: substrate phosphate (Arg) #status predicted <PTP3>

Query Match 40.7%; Score 709.5; DB 1; Length 1118;
 Best Local Similarity 48.0%; Pred. No. 7.e-53; Mismatches 95; Indels 3; Gaps 2;
 Matches 134; Conservative 47; MisMatches 95; Indels 3; Gaps 3;

Query 23 IKNQEGHMKQADANVLYSKYEELKGRNQSCDIALPENRGKRYNNLVDAT 82
 Db 802 IPADFDHTRKEDRSCDFPQDQYQLSIVGHSQSONVASYASENNAKKRYRULPYDWS 861

Query 83 RVKLNSVDDPDCSDYINASVYGNFRAYVTOCPLGKTDKDFKMMWQOMH 142
 Db 862 RYVLPKTHPFGSDYINASVYGNFRAYVTOCPLGKTDKDFKMMWQOMH 921

Query 143 QCVEKGRVKCDHWPADQDSLYKQDILQMLMSESTUPWTFKICGHEOLDA 201
 Db 922 NCMEAGRKVKCEHYWPLDSQFCTHLRLVTEEVMENWTFKELLQLOVEOKTLS--VR 979

Query 202 HRYTWPDPDGIVETRTOQFVPTVTDYINRSPGAGTVHCCAGVORTSF 261
 Db 980 QPHIQWAPDGHGVFSSPDILAPWMLRQMLQDQTMEGGPVPIWCSAQWGRGTRGMLADVLL 1039

Query 262 QDLSKDSVUVDVYGAVIDLHLRHRVHVMVOTECQVYVILHOCR 300
 Db 1040 RQLOSGEGLGPPFSVKKRQSRSPLMVOTECQVYVILHOCR 1078

Search completed: February 17, 2006, 01:25:38
 Job time : 43 secs

RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC
 DR EMBL: CABE1107048; CF89510.1; -; Genomic_DNA.
 DR InterPro: IPR003961; FN3_1.
 DR InterPro: IPR00397; TYR_Phosphatase.
 DR InterPro: IPR000387; TYR_PP.
 DR Pfam: PF00041; Fn3_1.
 DR Pfam: PF00102; Y_Phosphatase; 1.
 DR Prints: PRO700; PTYRIPHPTASE.
 DR SMART: SM0060; FN3_1.
 DR SMART; SM0136; PTFC; 1.
 DR SMART; SM0040; PTFC motif; 1.
 DR PROSITE; PSS0053; FN3_1.
 DR PROSITE; PSS0038; TYR_Phosphatase; 1.
 DR PROSITE; PSS0056; TYR_Phosphatase; 2; 1.
 DR PROSITE; PSS0055; TYR_Phosphatase_PP; 1.
 DR KW Hydrolase.
 FT NON_TER 1991 1991 1.
 FT SEQUENCE 1991 AA; 21280 MW; AEBCE4629DD27A78 CRC64;
 Best Local Similarity 67.5%; Score 1178.5; DB 2; Length 1991;
 Matches 213; Conservative 35; Mismatches 48; Indels 9; Gaps 1;
 Qy 9 LNLGOKGKAKTSCPKINGPSEGHHFKQASNSYVKEYELKQVGRNQSDIALPPE 69
 Db 1679 LLYVGVRSHNRVSPVKGQFOAHDDQDLSYSSSEFEDLQVGRNQAMVARVPEFN 1738
 Qy 69 GKNRNTNLYPTATRKLSDVDDPCDYINASITPGNFRREYVITPGPAGTQDKDFN 128
 Db 1739 GKNRNTNLYPTATRKLSDVDDPCDYINASITPGNFRREYVITPGPAGTQDKDFN 128
 Qy 129 MWIWEQVNRVWVQTCVVKRVKDHWPAQDSLYQDQDILQMSSESYLFWTREK 188
 Db 1799 MWIWEQVNRVWVQTCVVKRVKDHWPAQDSLYQDQDILQMSSESYLFWTREK 1849
 Qy 189 CGEBOGDALHRLTRHFTWPDQGVPETTOSLQFVRTVDRYIIRSPGAPTVWCSAQV 248
 Db 1850 SSESCAOPRRLHFTWPDQGVPETTOSLQFVRTVDRYIIRSPGAPTVWCSAQV 1909
 Qy 249 GRTGFIAIDRQLQDSDKSDVYDYGHDRLHRVAMQPECQVYHQCVDRYIARK 308
 Db 1910 GRTGFIAIDRQLQDSDKSDVYDYGHDRLHRVAMQPECQVYHQCVDRYIARK 1969
 Qy 309 LRSBO 313
 Db 1970 HRGEO_1974
 RESULT 7
 QW6V5 CHICK
 ID QW6V5--CHICK PRELIMINARY; PRT; 1406 AA.
 AC QW6V5;
 DT 01-NOV-1959 (TREMBL); 12, Created)
 DT 01-OCT-2001 (REMBL); 18, Last sequence update)
 DT 01-2003 (REMBL); 25, Last annotation update)
 DB Supporting cell antigen precursor.
 OC Gallus gallus (Chicken);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus gallus; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC NCBI_TAXID=9031;
 RN 111
 RN NUCLEOTIDE_SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=9929852; PubMed=10366616;
 RA Kruger R. P., Goodyear R. J., Legan P. K., Marchol M., Raphael Y.,
 Coranche D. A., Richardson G. P.;
 RA

RESULT 8
 PTTRJ HUMAN STANDARD; PRT; 1337 AA.
 ID PTTRJ_HUMAN STANDARD;
 AC 012931; Q1255; QHNM2;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase eta) (PTP-eta) (Protein-tyrosine phosphatase eta)
 DE tyrosine phosphatase receptor type J (Density enhanced phosphatase 1).
 DE DE (DPE-1) (CD148 antigen).
 GN Name=PTTRJ; Synonym=PTP-eta;
 OS Homo sapiens (Human);
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

		Best Local Similarity 55.7%; Pred. No. 6.5e-54;			
		Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;			
DR	GO: GO:0007507; P:heart development; IMP.	Qy	18 KTSCPKINQEGHMKLQADSNTYLSKEYELKQDGNSCQDIALPENRGKRYNLL 77	Db	917 KKSUURVNEEAFKKQDQNSCQFABEYELKQGKJLQISPKVTAELAENGKRYNVL 976
DR	GO: GO:001570; P:vasculogenesis; IMP.	Qy	78 PYDMDTRKSDNDOPCSDVYNASTPSNNPRKEYVTOGGLGPGKDFKRNWNEONHN 137	Db	977 PYDLSRVLKLS-VNHTSDYDYNANTPVGHSKDRFATQPLNTKDFRMWKRVYA 1035
DR	InterPro: IPR003961; FN III.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
DR	InterPro: IPR000387; TYR_PP.	Qy	78 PYDMDTRKSDNDOPCSDVYNASTPSNNPRKEYVTOGGLGPGKDFKRNWNEONHN 137	Db	977 PYDLSRVLKLS-VNHTSDYDYNANTPVGHSKDRFATQPLNTKDFRMWKRVYA 1035
DR	Pfam: PF0041; fnt_6.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
DR	PFam: PF00102; Y_phosphatase; 1.	Qy	78 PYDMDTRKSDNDOPCSDVYNASTPSNNPRKEYVTOGGLGPGKDFKRNWNEONHN 137	Db	977 PYDLSRVLKLS-VNHTSDYDYNANTPVGHSKDRFATQPLNTKDFRMWKRVYA 1035
DR	PRINTS: PRO00700; PTYPPHPTASE.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
DR	SMART: SM00194; PTPC; 1.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
DR	PROSITE: PS0033; TIR_PHOSPHATASE_1; 1.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
DR	PROSITE: PS0056; TYR_PHOSPHATASE_2; 1.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
KW	Glycoprotein; Hydrolase; Protein phosphatase; Repeat; Signal; Transmembrane.	FT	Potential.	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	SIGNAL	FT	Receptor-type tyrosine-protein phosphatase etc.	Db	977 PYDLSRVLKLS-VNHTSDYDYNANTPVGHSKDRFATQPLNTKDFRMWKRVYA 1035
FT	CHAIN	29	1238	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	TOPO_DOM	29	875	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	TOPO_DOM	898	1239	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	TRANSMEM	877	897	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	TOPO_DOM	40	130	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	DOMAIN	170	265	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	DOMAIN	267	354	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	DOMAIN	355	440	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	DOMAIN	442	527	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	DOMAIN	529	618	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	DOMAIN	620	712	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	DOMAIN	717	803	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	DOMAIN	942	1199	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	ACT_SITE	1140	1140	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	62	62	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	78	78	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	85	85	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	90	90	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	110	110	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	114	114	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	145	145	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	164	164	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	173	173	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	182	182	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	198	198	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	207	207	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	244	244	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	253	253	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	267	267	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	278	278	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	313	313	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	317	317	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	333	333	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	366	366	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	379	379	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	398	398	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	403	403	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	437	437	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	452	452	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	488	488	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	506	506	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	538	538	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	572	572	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	576	576	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	662	662	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	668	668	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	685	685	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	691	691	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
FT	CARBONYD	811	811	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
FT	CARBONYD	838	838	Db	1036 IVMUJQIENENTDVQIVYDLMRPLMVQEDQYVFLNQVLDIDRAK 1094
SEQUENCE	SEQUENCE	1238	AA;	Qy	138 IWMTOCQEKORVKDHWPADQDSLYQDILQMSLEVLPWTRFKECSEQDLAH 197
Query Match		49.8%; Score 868.5; DB 2; Length 1238; Best Local Similarity 55.7%; Pred. No. 6.5e-54; Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3; DR GO: GO:0007507; P:heart development; IMP. DR GO: GO:001570; P:vasculogenesis; IMP. DR InterPro: IPR003961; FN III. DR InterPro: IPR000387; TYR_PP. DR Pfam: PF0041; fnt_6. DR PRINTS: PRO00700; PTYPPHPTASE. DR SMART: SM00194; PTPC; 1. DR PROSITE: PS0033; TIR_PHOSPHATASE_1; 1.	1		

RA Shue B.C., Siden-Klains I., Simpson M., Skupski M.P., Smith T., DR InterPro: IPR003961; FN III.

RA Spier E., Spredlin A.C., Stapleton M., Strong R., Sun E., Wang X., DR InterPro: IPR003962; FNII subd.

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., DR InterPro: IPR003987; TTR Phosphatase.

RA Wang Z.-Y., Wasserman D.A., Weintraub G.M., Weissbach J., DR InterPro: IPR000242; Tyr_PP.

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., DR Pfam: PF00041; En3; 10.

RA Ye J., Yeh R.-P., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L., DR Pfam: PF00102; Y_phosphatase; 1.

RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O., DR Prints; PRO0014; PYRNPYPII.

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., DR Prints; PRO0070; PYRYPYPTASE.

RA Mirza S., Croby M.A., Mungall C.J., Matthews B.B., Campbell K.S., DR SMART; SM0060; Pnn; 11.

RA Hradecky P., Huang Y., Kainker J.S., Milburn G.H., Prochnik S.E., DR SWAP; SW00194; PTc; 1.

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayakkaroglu L., Berman B.P., DR PROSITE; PS00853; FN3; 11.

RA Bettencourt B.R., Ceolin M., Chiarini S.E., de Grey A.D.N.J., Drysdale R.A., DR PROSITE; PS00383; TYR_PHOSPHATASE_PTP; 1.

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., DR PROSITE; PS00056; TYR_PHOSPHATASE_PTP; 1.

RA Lewis S.E., DR PROSITE; PS00057; TYR_PHOSPHATASE_PTP; 1.

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review"; DR PROSITE; PS00058; TYR_PHOSPHATASE_PTP; 1.

RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002). DR PROSITE; PS00059; TYR_PHOSPHATASE_PTP; 1.

RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG). DR PROSITE; PS00060; TYR_PHOSPHATASE_PTP; 1.

RA STEPHAN-BERKELEY; TISSUE=embryo; DR PROSITE; PS00061; TYR_PHOSPHATASE_PTP; 1.

RA STAPLETON M., BROKATI P., HONG L., AGBAYINI A., CARLSON J.W., DR PROSITE; PS00062; TYR_PHOSPHATASE_PTP; 1.

RA CHAMPE M., CHAVEZ C., DORSETT V., DRESEN D., FRISE E., DR PROSITE; PS00063; TYR_PHOSPHATASE_PTP; 1.

RA GEORGE R.A., GONZALEZ M., GUAHAR H., KROMMELER B., LIU P.W., LIAO G., DR PROSITE; PS00064; TYR_PHOSPHATASE_PTP; 1.

RA MIRANDA A., MUNGALL C.J., NUÑO J., PACHEL J.M., PARGAS V., PARK S., DR PROSITE; PS00065; TYR_PHOSPHATASE_PTP; 1.

RA PAREL S., PHOAHANAVONG S., WAN K.H., YU C., LEWIS S.E., RUBIN G.M., DR PROSITE; PS00066; TYR_PHOSPHATASE_PTP; 1.

RA CELNIKAR S.E., DR PROSITE; PS00067; TYR_PHOSPHATASE_PTP; 1.

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases. DR PROSITE; PS00068; TYR_PHOSPHATASE_PTP; 1.

CC -!- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O = protein DR PROSITE; PS00069; TYR_PHOSPHATASE_PTP; 1.

CC -!- tyrosine + phosphate. DR PROSITE; PS00070; TYR_PHOSPHATASE_PTP; 1.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. DR PROSITE; PS00071; TYR_PHOSPHATASE_PTP; 1.

CC -!- ALTERNATIVE PRODUCTS: DR PROSITE; PS00072; TYR_PHOSPHATASE_PTP; 1.

CC -!- Event=Alternative splicing; Named isoforms=4; DR PROSITE; PS00073; TYR_PHOSPHATASE_PTP; 1.

CC -!- Name=Long; DR PROSITE; PS00074; TYR_PHOSPHATASE_PTP; 1.

CC -!- IsoId=p359592-1; Sequence=Displayed; DR PROSITE; PS00075; TYR_PHOSPHATASE_PTP; 1.

CC -!- Name=Short; DR PROSITE; PS00076; TYR_PHOSPHATASE_PTP; 1.

CC -!- IsoId=p359592-2; Sequence=VSP_005143; VSP_005144; DR PROSITE; PS00077; TYR_PHOSPHATASE_PTP; 1.

CC -!- Name=; DR PROSITE; PS00078; TYR_PHOSPHATASE_PTP; 1.

CC -!- IsoId=p359592-3; Sequence=VSP_015266; DR PROSITE; PS00079; TYR_PHOSPHATASE_PTP; 1.

CC -!- Note=No experimental confirmation available; DR PROSITE; PS00080; TYR_PHOSPHATASE_PTP; 1.

CC -!- Name=C; DR PROSITE; PS00081; TYR_PHOSPHATASE_PTP; 1.

CC -!- IsoId=p359592-4; Sequence=VSP_015264; VSP_015265; DR PROSITE; PS00082; TYR_PHOSPHATASE_PTP; 1.

CC -!- Note=No experimental confirmation available; DR PROSITE; PS00083; TYR_PHOSPHATASE_PTP; 1.

CC -!- TISSUE SPECIFICITY: Selectively expressed in anterior commissure and its junctions with the longitudinal tracts. DR PROSITE; PS00084; TYR_PHOSPHATASE_PTP; 1.

CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. DR PROSITE; PS00085; TYR_PHOSPHATASE_PTP; 1.

CC -!- Receptor class subfamily. DR PROSITE; PS00086; TYR_PHOSPHATASE_PTP; 1.

CC -!- SIMILARITY: Contains 12 fibronectin type-III domains DR PROSITE; PS00087; TYR_PHOSPHATASE_PTP; 1.

CC -!- SIMILARITY: Contains 1 tyrosine-protein phosphatase domain. DR PROSITE; PS00088; TYR_PHOSPHATASE_PTP; 1.

CC -!- This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. DR PROSITE; PS00089; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00090; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00091; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00092; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00093; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00094; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00095; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00096; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00097; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00098; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00099; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00100; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00101; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00102; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00103; TYR_PHOSPHATASE_PTP; 1.

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CC -!- DR PROSITE; PS00159; TYR_PHOSPHATASE_PTP; 1.

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CC -!- DR PROSITE; PS00265; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00266; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00267; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00268; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00269; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00270; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00271; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00272; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00273; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00274; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00275; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00276; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00277; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00278; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00279; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00280; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00281; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00282; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00283; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00284; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00285; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00286; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00287; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00288; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00289; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00290; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00291; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00292; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00293; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00294; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00295; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00296; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00297; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00298; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00299; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00300; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00301; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00302; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00303; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00304; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00305; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00306; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00307; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00308; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00309; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00310; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00311; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00312; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00313; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00314; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00315; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00316; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00317; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00318; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00319; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00320; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00321; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00322; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00323; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00324; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00325; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00326; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00327; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00328; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00329; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00330; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00331; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00332; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00333; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00334; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00335; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00336; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00337; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00338; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00339; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00340; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00341; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00342; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00343; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00344; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00345; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00346; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00347; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00348; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00349; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00350; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00351; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00352; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00353; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00354; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00355; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00356; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00357; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00358; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00359; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00360; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00361; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00362; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00363; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00364; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00365; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00366; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00367; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00368; TYR_PHOSPHATASE_PTP; 1.

CC -!- DR PROSITE; PS00369; TYR_PH

QY 82 TRVQLSNVDDPCSDYINASVLPGNHPRREYVITQGPLUGTKDPPKQAVWENVINTNV 141
Db 1311 SRFKLOQPVDDGSDVINYVGHNSPRFINTQGLHSTRDPWNCWSRATNL 1370
QY 142 TQCVERKGRVKCIPHYMPADODSLYYGDMILLOMABSVIPENWTFIREFKIC-GBEOLDAHRL 200
Db 1371 TRCEPKGREKCOYMPNDTVPVYGDVKVQIANDSHADWMTEFMLCRGSEB- -RIL 1426
QY 201 RHFHTVMPDHGPETTOSLIQFRTVDYINRSPGKPTWHSASJGRGTFALDR 260
Db 1427 RHFHTTWPDRGVPNPQTLIREVRAFRDRIGAB- -ORPTVHCSAGVGRSGTFITLDR 1484
QY 261 LQDSDSKSYVYGAVIDLRLHRYHMQECPVYHQCYRDVURARK 308
Db 1485 LQINTSDYVQIYAMRKERVWWVQOYICHOCLLAVLEGKE 1532

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